

FIG. 1A

1 CCCACGCGTCCGGGGAGCTTGCACTAACATCTACAATGGCTTCTAAAAAGCACAGATGAC 60
 61 CTGCTACACTTCCTGACTTGCTTGCTATTGGTTGGCACTGTTCATAAATATAAATTGCTC 120
 121 TTTCACCTTTCTTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA 180
 181 GAGGCAGCAGAAGCCAGGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG 240
 241 CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTTGAC 300
 301 TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCATTTGAT 360
 361 AAGGGAAAAC TAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT 420
 421 GTGAGCAACGTGGAAGATGGGTGATTTCTGCATTTCCAAC TGAGCATGGAGAGAAAAATT 480
 481 TATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA 540
 1 M E P N G T F S N 9
 541 TAACAACAGCAGGAAC TGACAATTGAAAAC TTCAAGAGAGAATTTTCCCAATTGTATA 600
 10 N N S R N C T I E N F K R E F F P I V Y 29
 601 TCTGATAATATTTTCTGGGAGTCTTGGGAAATGGGTGTCCATATATGTTTCTCTGCA 660
 30 L I I F F W G V L G N G L S I Y V F L Q 49
 661 GCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTGGCCATTTTCAGATCT 720
 50 P Y K K S T S V N V F M L N L A I S D L 69
 721 CCTGTTTATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGAT 780
 70 L F I S T L P F R A D Y Y L R G S N W I 89
 781 ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAG 840
 90 F G D L A C R I M S Y S L Y V N M Y S S 109
 841 TATTTATTTCTGACCGTGTGAGTGTGTGCGTTTCTGGCAATGGTTACCCCTTTTCG 900
 110 I Y F L T V L S V V R F L A M V H P F R 129

FIG. 1B

901 GCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCT 960
 130 L L H V T S I R S A W I L C G I I W I L 149
 961 TATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTAC 1020
 150 I M A S S I M L L D S G S E Q N G S V T 169
 1021 ATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGC 1080
 170 S C L E L N L Y K I A K L Q T M N Y I A 189
 1081 CTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCAT 1140
 190 L V V G C L L P F F T L S I C Y L L I I 209
 1141 TCGGGTTCTGTAAAAAGTGGAGGTCCCAGAAATCGGGGCTGCGGGTTTCTCACAGGAAGGC 1200
 210 R V L L K V E V P E S G L R V S H R K A 229
 1201 ACTGACCACCATCATCATCACCTTGATCATCTTCTTCTGTGTTTCTGCCCCTATCACAC 1260
 230 L T T I I I T L I I F F L C F L P Y H T 249
 1261 ACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAA 1320
 250 L R T V H L T T W K V G L C K D R L H K 269
 1321 AGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTA 1380
 270 A L V I T L A L A A A N A C F N P L L Y 289
 1381 TTACTTTGCTGGGAGAAATTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCC 1440
 290 Y F A G E N F K D R L K S A L R K G H P 309
 1441 ACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTAGTGTGTGGTTGAGAAAGGAAACAAG 1500
 310 Q K A K T K C V F P V S V W L R K E T R 329
 1501 AGTATAAGGAGCTCTTAGATGAGACCTGTCTTGTATCCTTGTGTCCATCTTCATTCAC 1560
 330 V * 331
 1561 CATAGTCTCCAAATGACTTTGTATTTACATCACTCCCAACAAATGTTGATTCTTAATATT 1620
 1621 TAGTTGACCATTACTTTTGTAAATAAGACCTACTTCAAAAATTTTATTCAGTGTAACAAA 1680
 1681 AAAAAAAAAAAAAAAAAAAAAAAAAA 1708

FIG. 2A

		1		50
HGPRBMY11	(1)	-----MSLQPSIIVSEIEPNC-----	TFNNNSRNC	EN--FI
HGPRBMY11v1	(1)	MERKFMSLQPSIIVSEIEPNC-----	TFNNNSRNC	EN--FI
P2Y5_CHICK	(1)	-----MSSNCITED--FI		
P2YR_CHICK	(1)	MTEALISAAALNGQPELAGG-----	WAGNATKCTKTCGF	
P2YR_MELGA	(1)	MTEALISAAALNGQPELAGG-----	WAGNATKCTKTCGF	
P2YR_RAT	(1)	MTEVPWSAVPNGDAAALAGLGLWGNSTIAS	IAVVSFRCP	IKTCGF
Q9Y271	(1)	-----MDETG-----	NLTVSSAT	CHDTIDDF
GPRH_HUMAN	(1)	-----MNGLEVAPP-----	LTINFSL	AEOQGQETP
		51		100
HGPRBMY11	(22)	REERPIVYELFFWCVLGNGLSIYEFQPKKKS	SVVMENLA	ADLL
HGPRBMY11v1	(38)	REERPIVYELFFWCVLGNGLSIYEFQPKKKS	SVVMENLA	ADLL
P2Y5_CHICK	(14)	YTFGCVESWVFECGANCVAIYEFATLVRNE	SVVMENLA	ADLL
P2YR_CHICK	(40)	EYVLPVYELVFLIGFLGNSVAIMFVHMPWSS	SVVMENLA	ADLL
P2YR_MELGA	(40)	EYVLPVYELVFLIGFLGNSVAIMFVHMPWSS	SVVMENLA	ADLL
P2YR_RAT	(51)	EYVLPVYELVFLIGFLGNSVAIMFVHMPWSS	SVVMENLA	ADLL
Q9Y271	(23)	NQVYSTLYSMESVYGFEGNCPVAYVYKTK	SVVMENLA	ADLL
GPRH_HUMAN	(31)	NMERASPVLLDFIEIYVGNLALDFERDHS	SVVMENLA	ADLL
		101		150
HGPRBMY11	(72)	ESTLPLFRADYYIRGNNWIFGDEACHMS	SVVMYSS	IFLTVSVVRF
HGPRBMY11v1	(88)	ESTLPLFRADYYIRGNNWIFGDEACHMS	SVVMYSS	IFLTVSVVRF
P2Y5_CHICK	(64)	VEFLPFRIRYIEVVRN--WPGDVLC	SVTFY	FNMYGSILFLTCISVDRF
P2YR_CHICK	(90)	VLTLPALIEYYFNKIDWIFGDMCKLQRF	IEVNEVGSILFLTCISVHR	
P2YR_MELGA	(90)	VLTLPALIEYYFNKIDWIFGDMCKLQRF	IEVNEVGSILFLTCISVHR	
P2YR_RAT	(101)	VLTLPALIEYYFNKIDWIFGDMCKLQRF	IEVNEVGSILFLTCISVHR	
Q9Y271	(73)	VCLPLRVVYVHKGILWFGDFICRIST	VAIVNEVYCSIEFMTAS	SFFRC
GPRH_HUMAN	(81)	VVLPLTRIVYHFGSNHWPFCETACRIT	GFEFYENMYASTY	FLTCISADRF
		151		200
HGPRBMY11	(122)	LAMVHPRKLLHYTSIRSAWITCGITNILL	MASSIM	ELDS---CSEONGSV
HGPRBMY11v1	(138)	LAMVHPRKLLHYTSIRSAWITCGITNILL	MASSIM	ELDS---CSEONGSV
P2Y5_CHICK	(113)	LAIVHPRKSKTRIRRNARIVCVAWITVE	AGSTPASE	FQSTIRQNTTEQ
P2YR_CHICK	(140)	TGVVHPLKSLGRKKKNNAVYVSSLVVAL	VVAIAPILE	FVSGTCVRENKTK
P2YR_MELGA	(140)	TGVVHPLKSLGRKKKNNAVYVSSLVVAL	VVAIAPILE	FVSGTCVRENKTK
P2YR_RAT	(151)	SGVVYPLKSLGRKKKNNAVYVSSLVVAL	VVAIAPILE	FVSGTCVRENKTK
Q9Y271	(123)	IAIVFVONINLVYOKKARFVCGVITFV	ILTSPE	MAKPQKDEKNNK
GPRH_HUMAN	(131)	LAIVHPVKSLKERRPLYAHIACARL	MAVAVAMAPL	LVSPQTVQTNNTV
		201		250
HGPRBMY11	(169)	TSCLE--LNLYKIAKQOMNYIALVVGCL	EPFENST	CYLLIIRVLEKVE
HGPRBMY11v1	(185)	TSCLE--LNLYKIAKQOMNYIALVVGCL	EPFENST	CYLLIIRVLEKVE
P2Y5_CHICK	(163)	RTCFENFPFESTIKTYISRIYIEI	VGFFIPI	ENNTCSTIRALNRP
P2YR_CHICK	(190)	TCYDT--TADEYRSYFYVSMCTTFMFC	CIPIFIV	IGCYGLIYALYK
P2YR_MELGA	(190)	TCYDT--TADEYRSYFYVSMCTTFMFC	CIPIFIV	IGCYGLIYALYK
P2YR_RAT	(201)	TCYDS--TSDEYRSYFYVSMCTTFMFC	CIPIFIV	IGCYGLIYALYK
Q9Y271	(173)	CFEPP--QDNQTKNHLYLHYVSL	FVGFIIP	IVCYTMITLILKK
GPRH_HUMAN	(181)	CLQLY-----REKISHH	YVSL	LAFAFTPPIITTCYLLIIRSLRGL

FIG. 2B

		251		300
HGPRBMY11	(217)	MPESGLRVSHRKA	TTIIITLI	IFFFPLPYHRTIL-----TIWK
HGPRBMY11v1	(233)	MPESGLRVSHRKA	TTIIITLI	IFFFPLPYHRTIL-----TIWK
P2Y5_CHICK	(213)	ILSRNKLS-KKKY	KKTHH	VLECFEPPYTLISLMS--TOTWIN
P2YR_CHICK	(238)	EDNSPLR---	RKSTIYNTIIVLT	TFAMSLPPEHVNRTILRARLDFOTPO
P2YR_MELGA	(238)	EDNSPLR---	RKSTIYNTIIVLT	TFAMSLPPEHVNRTILRARLDFOTPO
P2YR_RAT	(249)	EDNSPLR---	RKSTIYNTIIVLT	TFAMSLPPEHVNRTILRARLDFOTPE
Q9Y271	(221)	HKKNLSS--HKKA	IGMIMVTA	AFLVSEMPYHRTILHFLHN--ETKP
GPRH_HUMAN	(224)	RVEKRLE---	TKGRMTAIVLA	IFLVGFPPYHVNRTILHYR--HGAS
		301		350
HGPRBMY11	(261)	GLCKDRHKKLV	ITLALANACFNP	ILYFACIFRLSALRKGHP
HGPRBMY11v1	(277)	GLCKDRHKKLV	ITLALANACFNP	ILYFACIFRLSALRKGHP
P2Y5_CHICK	(260)	GSVVTATMTM	PTLSTAVSNCC	FDPIVYFEDTNSLD--K--V
P2YR_CHICK	(285)	CAFNDKIVAIYQ	YTRGLASLNS	SCVDPILYFAGDTFRRLSRATRKSSR
P2YR_MELGA	(285)	CAFNDKIVAIYQ	YTRGLASLNS	SCVDPILYFAGDTFRRLSRATRKSSR
P2YR_RAT	(296)	CAFNDKIVAIYQ	YTRGLASLNS	SCVDPILYFAGDTFRRLSRATRKASR
Q9Y271	(267)	QDSVLRMQKSVV	ITLSLAASNC	CFDPILYFFSCAFRRLS--FRKHSL
GPRH_HUMAN	(269)	QATORIHALANR	ITSLTSLNGAL	DPIMYFFAFRRLS--FRKHSL
		351		379
HGPRBMY11	(311)	KAK-TKCVF	EVSWLRKE	TEV-----
HGPRBMY11v1	(327)	KAK-TKCVF	EVSWLRKE	TEV-----
P2Y5_CHICK	(306)	QNT-----		
P2YR_CHICK	(335)	SEP-NVQSKSE	MTLNILTEYK	QNGDTSL
P2YR_MELGA	(335)	SEP-NVQSKSE	MTLNILTEYK	QNGDTSL
P2YR_RAT	(346)	SEA-NLQSKSE	MTLNILSEFK	QNGDTSL
Q9Y271	(316)	SVT-YVPRK	KASLPEKGE	EICKV-----
GPRH_HUMAN	(319)	GPPPSFEGKT	NSSLSAKSEL	-----

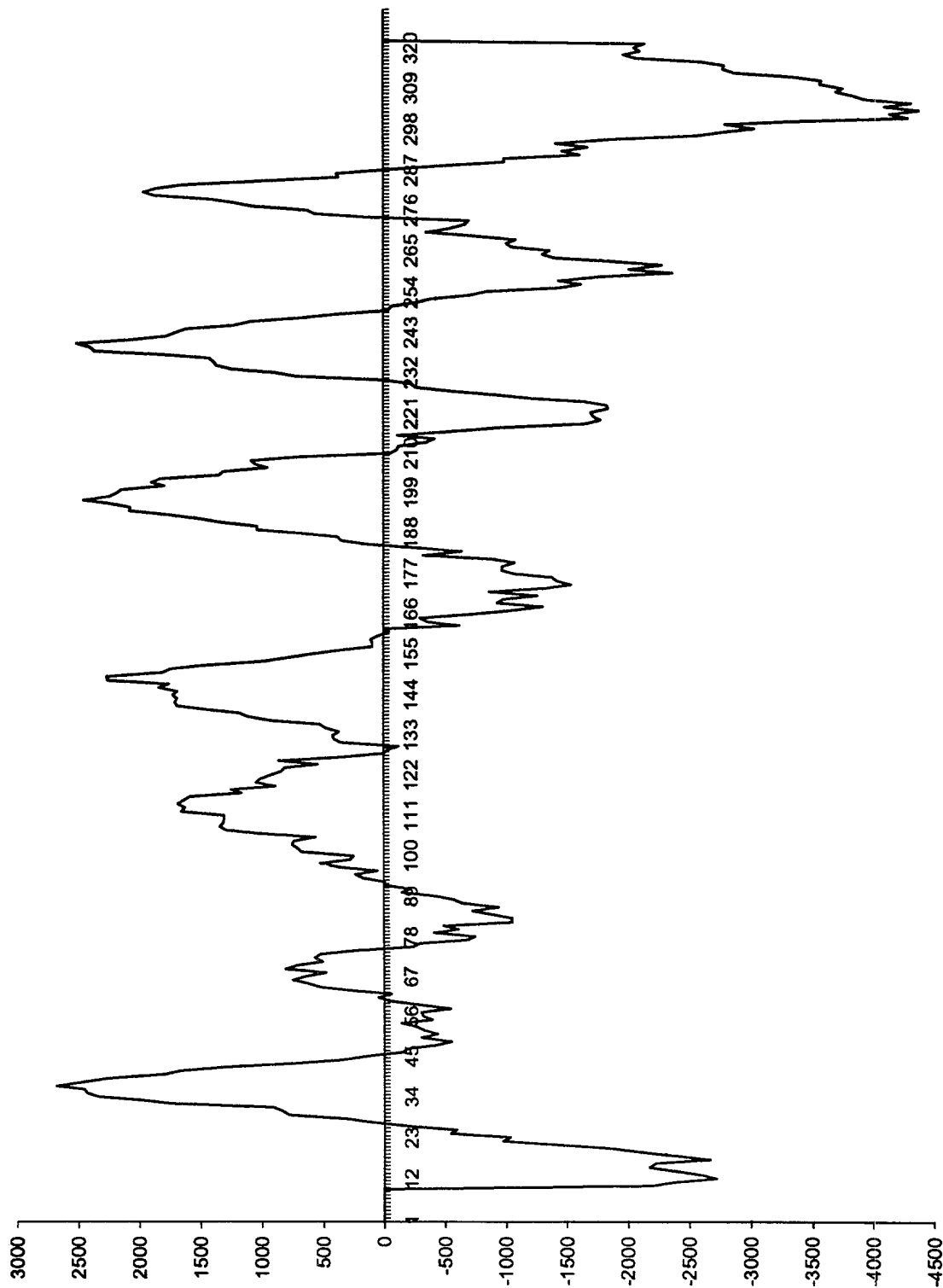


FIG. 3

FIG. 4

Expression Profiling of Novel Human GPCR, HGPRBMY11

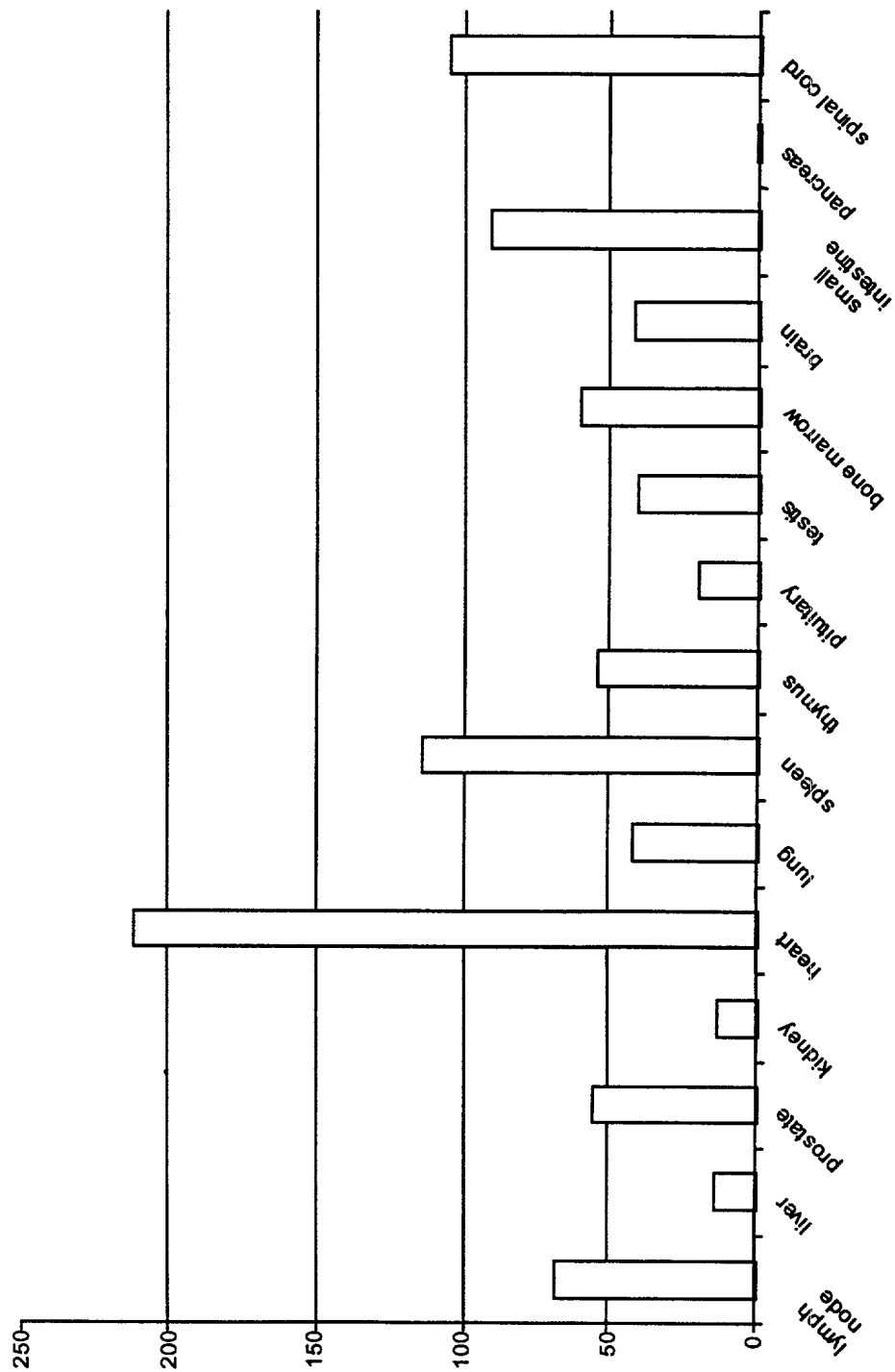


FIG. 5

HGPRBMY11

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human cysteinyl leukotriene receptor	gi 11422069	37%	49%
chick purinergic receptor 5	gi P32250	36%	46%
human G-protein-coupled receptor GPR17	gi Q13304	36%	46%
chick purinergic receptor	gi P34996	30%	45%
turkey purinergic receptor	gi P49652	30%	45%
rat purinergic receptor	gi P49651	30%	44%

HGPRBMY11v1

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human cysteinyl leukotriene receptor	gi 11422069	37.2%	49%
chick purinergic receptor 5	gi P32250	36.7%	46.1%
human G-protein-coupled receptor GPR17	gi Q13304	36.2%	46.1%
chick purinergic receptor	gi P34996	29.5%	43.9%
turkey purinergic receptor	gi P49652	29.8%	44.2%
rat purinergic receptor	gi P49651	29.6%	44%

FIG. 6A

1	ATGGAGAGAAAATTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT	60
1	M E R K F M S L Q P S I S V S E M E P N	20
61	GGCACCTTCAGCAATAACAACAGCAGGAACGCACAATTGAAAACCTCAAGAGAGAATTT	120
21	G T F S N N N S R N C T I E N F K R E F	40
121	TTCCCAATTGTATATCTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA	180
41	<u>F P I V Y L I I F F W G V L G N G L S I</u>	60
181	TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTG	240
61	<u>Y V F L</u> Q P Y K K S T S V N <u>V F M L N L</u>	80
241	GCCATTTTCAGATCTCCTGTTCATAAGCAGCCTTCCCTTCAGGGCTGACTATTATCTTAGA	300
81	<u>A I S D L L F I S T L P F R A D Y Y L R</u>	100
301	GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTC	360
101	G S N W I F G D L A C R I M S Y S L Y V	120
361	AACATGTACAGCAGTATTTATTTCTGACCGTGCTGAGTGTGTGCGTTTCTGGCAATG	420
121	<u>N M Y S S I Y F L T V L S V V R F L A M</u>	140
421	GTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGG	480
141	<u>V H P F R L L H V T S I R S</u> <u>A W I L C G</u>	160
481	ATCATATGGATCCTTATCATGGCTTCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG	540
161	<u>I I W I L I M A S S I M L L</u> D S G S E Q	180
541	AACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC	600
181	N G S V T S C L E L N L Y K <u>I A K L Q T</u>	200
601	ATGAACTATATTGCCTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGT	660
201	<u>M N Y I A L V V G C L L P F F T L S I C</u>	220
661	TATCTGCTGATCATTCGGGTTCTGTAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTT	720
221	<u>Y L</u> L I I R V L L K V E V P E S G L R V	240
721	TCTCACAGGAAGGCACTGACCACCATCATCATCACCTTGATCATCTTCTTCTGTGTTTC	780
241	S H R K <u>A L T T I I I T L I I F F L C F</u>	260
781	CTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAA	840
261	<u>L P Y H T L</u> R T V H L T T W K V G L C K	280
841	GACAGACTGCATAAAGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTC	900
281	D R L H K <u>A L V I T L A L A A A N A C F</u>	300

FIG. 6B

901 AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTAAGGACAGACTAAAGTCTGCACTC 960
301 N P L L Y Y F A G E N F K D R L K S A L 320

961 AGAAAAGGCCATCCACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTAGTGTGTGGTTG 1020
321 R K G H P Q K A K T K C V F P V S V W L 340

1021 AGAAAGGAAACAAGAGTATAA 1041
341 R K E T R V 346

FIG. 7

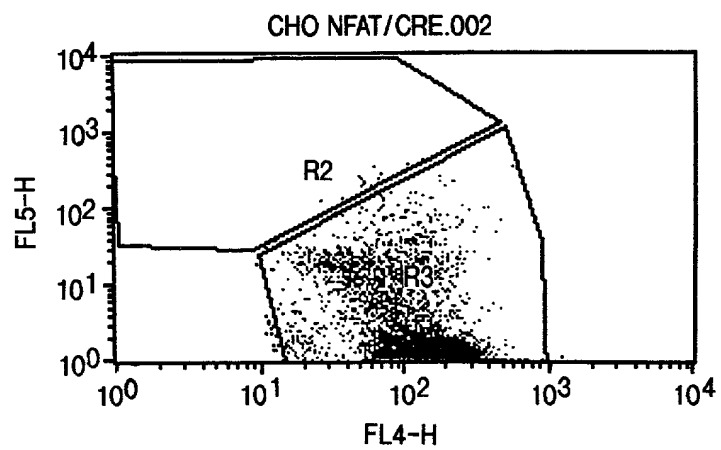


FIG. 8

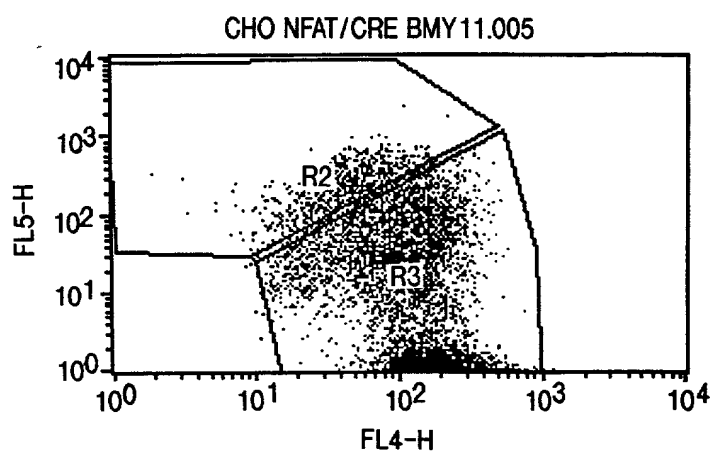


FIG. 9

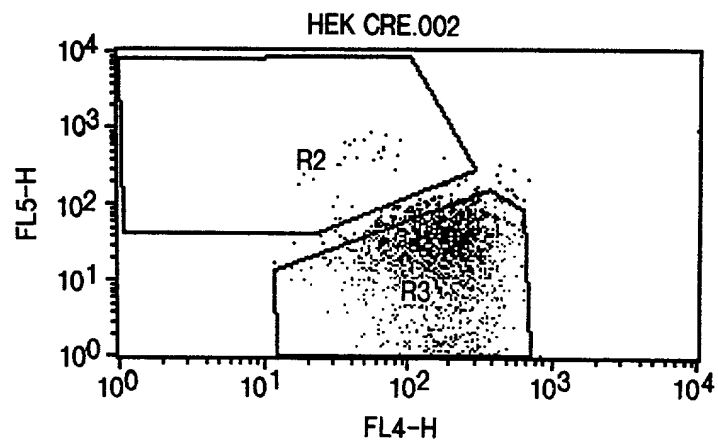


FIG. 10

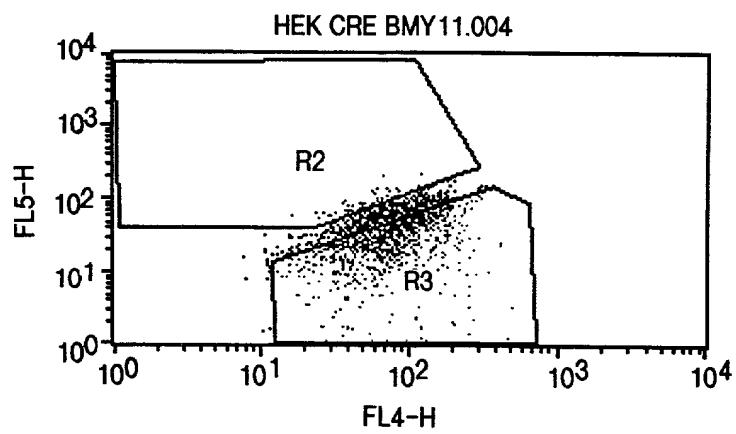


FIG. 11

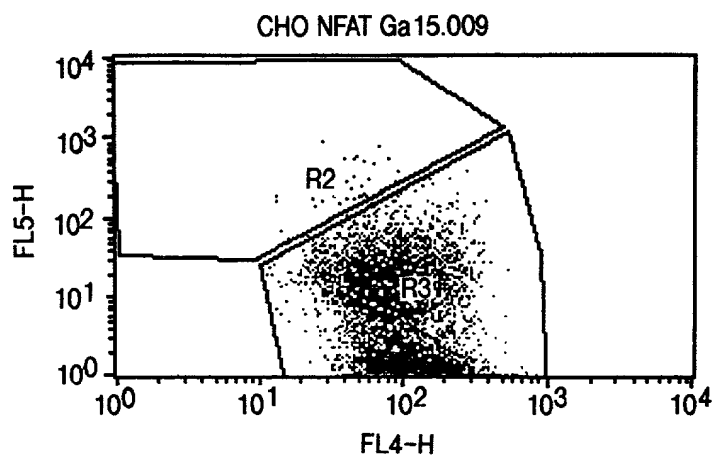


FIG. 12

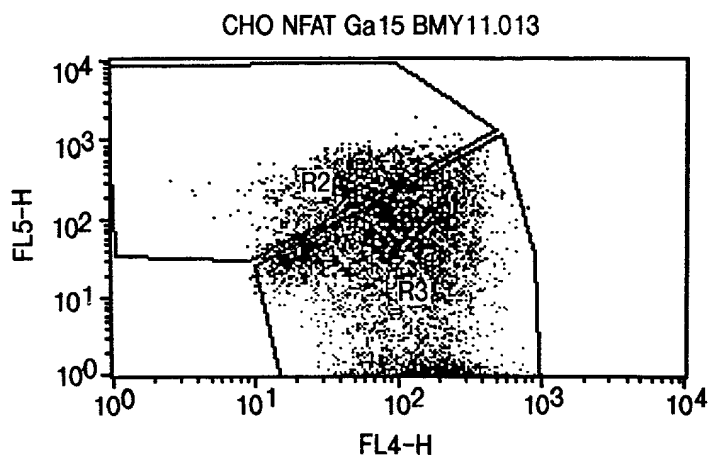


FIG. 13

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)



Cho NFAT Ga15 BMY11 (Fluorescent vs. Bright Field)



FIG. 14a

Cho-NFAT CRE

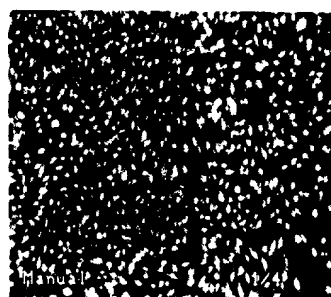


FIG. 14b

Cho-NFAT CRE + F/T/P

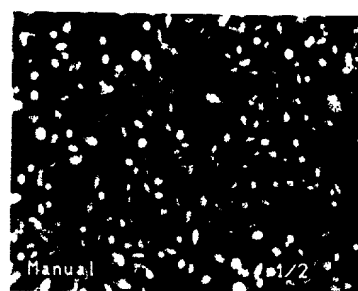


FIG. 14c

Cho-NFAT CRE oGPCR-Intermediate

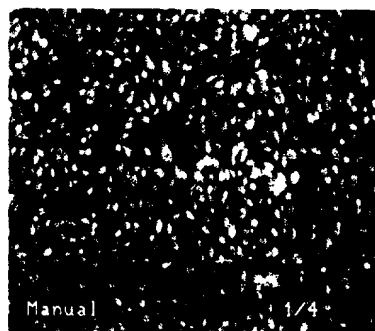


FIG. 14d

Cho-NFAT CRE oGPCR High

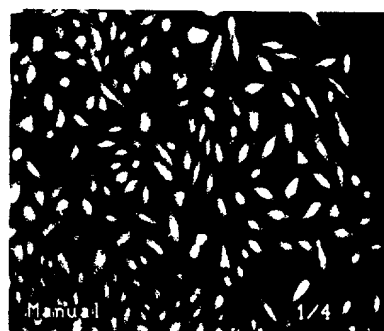


FIG. 15A

1 ATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT 60
1 M S L Q P S I S V S E M E P N G T F S N 20

61 AACAAACAGCAGGAACCTGCACAATTGAAAACCTCAAGAGAGAATTTTCCCAATTGTATAT 120
21 N N S R N C T I E N F K R E F F P I V Y 40

121 CTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTCTCCTGCAG 180
41 L I I F F W G V L G N G L S I Y V F L Q 60

181 CCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTTCAGATCTC 240
61 P Y K K S T S V N V F M L N L A I S D L 80

241 CTGTTTCATAAGCAGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA 300
81 L F I S T L P F R A D Y Y L R G S N W I 100

301 TTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAGT 360
101 F G D L A C R I M S Y S L Y V N M Y S S 120

361 ATTTATTTCTGACCGTCTGAGTGTGTGCGTTTCTGGCAATGGTTCACCCCTTTTCGG 420
121 I Y F L T V L S V V R F L A M V H P F R 140

421 CTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT 480
141 L L H V T S I R S A W I L C G I I W I L 160

481 ATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTACAC 540
161 I M A S S I M L L D S G S E Q N G S V T 180

541 TCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACATATATTGCC 600
181 S C L E L N L Y K I A K L Q T M N Y I A 200

601 TTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCATT 660
201 L V V G C L L P F F T L S I C Y L L I I 220

661 CGGGTTCTGTAAAGTGGAGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCA 720
221 R V L L K V E V P E S G L R V S H R K A 240

721 CTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTCTGCCCTATCACACA 780
241 L T T I I I T L I I F F L C F L P Y H T 260

781 CTGAGGACCTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAAA 840
261 L R T V H L T T W K V G L C K D R L H K 280

841 GCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTAT 900
281 A L V I T L A L A A A N A C F N P L L Y 300

0399123E-03130

FIG. 15B

901 TACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCA 960
301 Y F A G E N F K D R L K S A L R K G H P 320

961 CAGAAGGCAAAGACAAAGTGTGTTTCCCTGTAGTGTGTGGTTGAGAAAGGAAACAAGA 1020
321 Q K A K T K C V F P V S V W L R K E T R 340

1021 GTATAA 1026
341 V 341